

Fig. 1.

Fig. 2.

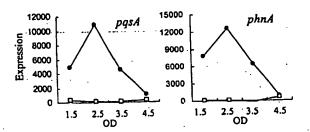


Fig. 3

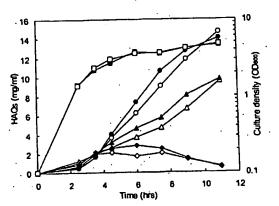


Fig. 4.

Fig. 5.

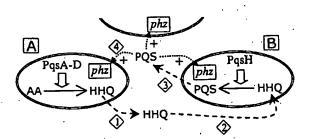


Fig. 6.

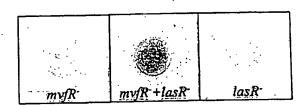


Fig. 7.

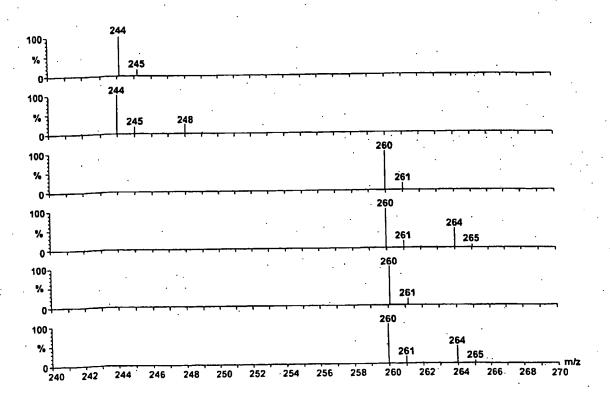


Fig. 8.

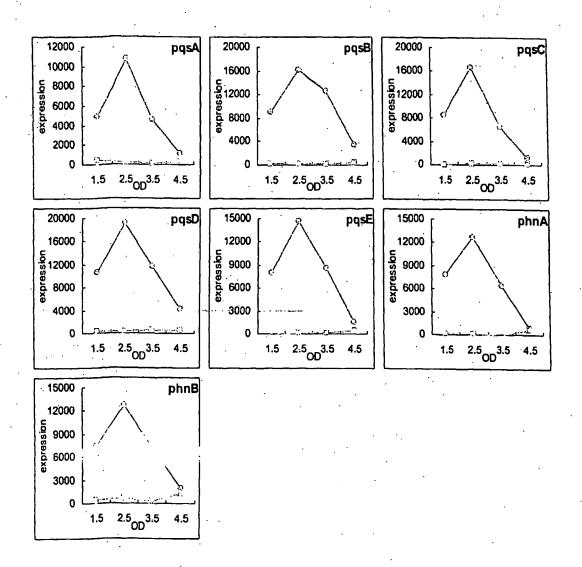


Fig. 9.

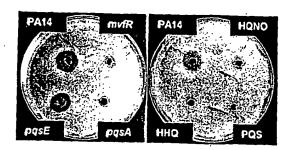


Fig. 10.

All sequences are from Pseudomonas aeruginosa

pqsA (SEQ ID NO:1)

ATGTCCACATTGGCCAACCTGACCGAGGTTCTGTTCCGCCTCGATTTCGATCCCGATACCGCCGTTTATCA GCCTGCATCGCGGTCGGCGCCATTCCCGCCGTGATCAATCCCAAGTCCCGCGAGCAGGCCCTGGCCGATAT GCGGACCTCGATTGGAGTGCCTTCCATCGCCAGGACCCGGCGGCAGCCTGTTTCCTGCAATACACCTCGGG TTCCACCGGGGCGCCCAAGGGGGTGATGCACAGCCTGCGCAACACGCTCGGTTTCTGCCGGGCGTTCGCTA CGGAGTTGCTGGCATTGCAGGCGGGAGACCGGCTGTATTCGATTCCCAAGATGTTCTTCGGCTATGGCATG GGCAACAGCCTGTTCTTTCCCTGGTTCAGCGGAGCCTCGGCGCTGCTCGACGATACCTGGCCGAGCCCGGA GCGGGTTCTGGAGAACCTGGTCGCCTTCCGCCCCCGGGTCCTGTTTGGGGTGCCGGCCATCTATGCCTCGC TGCGTCCGCAGGCCAGGGAGCTGTTGAGCAGCGTGCGCCTGGCGTTTTCCGCCGGCTCGCCGCTGCCGCGC GGCGAGTTCGAATTCTGGGCCGCACGGGCTGGAGATCTGCGACGCATCGGGGCTACCGAGGTCGGCCA TGTGTTCCTCGCCAACCGCCCGGGCCAGGCGCGTGCCGACAGCACCGGGCTGCCGTTGCCTGGCTATGAGT GCCGGCTGGTGGACCGCGAAGGACACTATCGAGGAAGCGGGCCGGCAAGGCGTGCTGTTGGTGCGTGGC CCAGGGCTGAGTCCGGGTTACTGGCGGGCCAGCGAAGAGCAGCAGCGCGCTTCGCAGGTGGCTGCTACCG CACCGGCGACCTGTTCGAGCGCGACGAGTCGGGTGCCTACCGTCACTGTGGGCGGGAAGACGATCTGTTCA AGGTGAATGGCCGCTGGGTGCTGCCGACCCAGGTCGAGCAGCCATCTGCCGTCATCTGCCGGAAGTGAGC GAGGCGGTTCTGGTTCCTACCTGCCGGCTGCACGACGGCTTGCGTCCGACCCTGTTCGTCACCCTGGCCAC TCCGCTGGACGACAACCAGATCCTGCTGGCGCAGCGCATCGACCAGCATCTCGCCGAACAGATTCCCTCGC GAGCTGCGCCACCTGGCCGACACCCTTTATCACGACAACCTTCCGGAGGAACGGGCATGTTGA

pqsB (SEQ ID NO:2)

pqsC (SEQ ID NO:3)

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pqsD (SEQ ID NO:4)

pqsE (SEQ ID NO:5)

pasH (SEO ID NO:6)

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pqsL (SEQ ID NO:7)

ATGACGGACAACCATATCGATGTACTGATCAACGGCTGCGGCATCGGCGGGGCGATGCTCGCCTACCTGCT CGGCCGCGGGGCCACCGCGTGGTGGTAGTGGAACAGGCACGGCGCGAACGCGCGATCAACGGCGCCGACC TGCTCAAGCCGGCCGCATCCGGGTGGTCGAGGCGGCCGGGTTGTTGGCCGAGGTGACCCGTCGCGGTGGG CGGGTCCGCCATGAGCTGGAGGTCTATCACGACGCGAGCTGCTTCGCTATTTCAACTATTCCAGCGTCGA CGCGCGCGCTATTTCATCCTCATGCCCTGCGAGTCGCTGCGCCCTGGTACTGGAAAAAATCGACGGCG CAGGTGCGCCTGAACGACGGCCGCGTGCTGCGTCCGCGGGTGGTGGTGGGAGCCGACGGTATCGCCTCCTA CGTGCGCCGCCGGCTGCTCGATATCGATGTGGAACGCCGCCCCTACCCGTCGCCGATGCTGGTCGGCACCT TATCCGATCGGTTTCGACCGCGCGCGACTGGTGGTGAGCTTCCCCAGGGAGGAGGGCGCGCGAGCTGATGGC CGACACCCGCGGCGAGTCGCTGCGCCGCGCTTGCAACGCTTCGTCGGCGACGAGAGCGCCGAGGCGATCG CCGCCGTCACCGGCACTTCGCGCTTCAAGGGCATCCCCATCGGCTACTGAACCTGGACCGCTACTGGGCG GACAACGTGGCGATGCTCGGCGACGCCATCCACAACGTGCATCCGATCACCGGCCAGGGCATGAACCTGGC CATCGAGGACGCCAGCGCCTGGCCGACGCCTCGACCTGGCCTTGCGCGACGCCTGCGCGCTGGAGGATG CCCTGGCCGGCTACCAGGCCGAGCGCTTCCCGGTGAACCAGGCGATCGTCTCCTATGGCCATGCGTTGGCC ACCAGCCTGGAGGATCGCCAGCGCTTCGCCGGGGTCTTCGACACCGCCCTGCAGGGCAGCAGCCGTACGCC GGAAGCCCTGGGCGGCGAGCGCTCCTACCAGCCGGTGCGGTCGCCGGCGCCGCTCGGCTGA

PgsA (SEQ ID NO:8)

MSTLANLTEVLFRLDFDPDTAVYHYRGQTLSRLQCRTYILSQASQLARLLKPGDRVVLALNDSPSLACLFL ACIAVGAIPAVINPKSREQALADIAADCQASLVVREADAPSLSGPLAPLTLRAAAGRPLLDDFSLDALVGP ADLDWSAFHRQDPAAACFLQYTSGSTGAPKGVMHSLRNTLGFCRAFATELLALQAGDRLYSIPKMFFGYGM GNSLFFPWFSGASALLDDTWPSPERVLENLVAFRPRVLFGVPAIYASLRPQARELLSSVRLAFSAGSPLPR GEFEFWAAHGLEICDGIGATEVGHVFLANRPGQARADSTGLPLPGYECRLVDREGHTIEEAGRQGVLLVRG PGLSPGYWRASEEQQARFAGGWYRTGDLFERDESGAYRHCGREDDLFKVNGRWVVPTQVEQAICRHLPEVS EAVLVPTCRLHDGLRPTLFVTLATPLDDNQILLAQRIDQHLAEQIPSHMLPSQLHVLPALPRNDNGKLARA ELRHLADTLYHDNLPEERAC

PasB (SEO ID NO:9)

MLIQAVGVNLPPSYVCLEGPLGGERPRAQGDEMLMQRLLPAVREALDEAAVKPEEIDLIVGLALSPDHLIE NRDIMAPKIGHPLQKVLGANRAHVFDLTDSSLARALYVVDTLASDQGYRNVLVVRGESSQGLEVDSESGFA LADGALALLCRPTGKAAFRRGALGGDPAQEWLPLSIPLNTDIRQVGDVKGHLNLPAQPGLPEAVRAGFTRL AGDFPOLNWVREEWFGOGRPDGRCLGPFELASQLRAAQRDRLDELLLISFDPFGMVVEGVTLELAGEAHA

PqsC (SEQ ID NO:10)

MHKVKLAAITCELPARSYENDDPVFAAVPDLSESWWQFWGVNRRGYFDPRNGENEFSLVVRAAERLLRSSD TAPDSVDMLICSASSPIMTDAGDVLPDLRGRLYPRMANVLSKQLGLSRALPLDSQMECASFLLNLRLAASM IRQGKAEKVLVVCSEYISNLLDFTSRTSTLFADGCAVALLTRGDDDSCDLLASAEHSDATFYEVATGRWRL PENPTGEAKPRLYFSLFSDGQNKMASFVPTNVPIAMRRALEKAGLGSDDIDYFVFHQPAPFLVKAWAEGIG ARPEQYQLTMGDTGVMISVSIPYTLMTGLREGKIRPGDRIVMAGAATGWGFAAQVWQLGEVLVC

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PqsD (SEQ ID NO:11)

MGNPILAGLGFSLPKRQVSNHDLVGRINTSDEFIVERTGVRTRYHVEPEQAVSALMVPAARQAIEAAGLLP EDIDLLLVNTLSPDHHDPSQACLIQPLLGLRHIPVLDIRAQCSGLLYGLQMARGQILAGLARHVLVVCGEV LSKRMDCSDRGRNLSILLGDGAGAVVVSAGESLEDGLLDLRLGADGNYFDLLMTAAPGSASPTFLDENVLR EGGGEFLMRGRPMFEHASQTLVRIAGEMLAAHELTLDDIDHVICHQPNLRILDAVQEQLGIPQHKFAVTVD RLGNMASASTPVTLAMFWPDIOPGORVLVLTYGSGATWGAALYRKPEEVNRPC

PqsE (SEQ ID NO:12)

MLRLSAPGQLDDDLCLLGDVQVPVFLLRLGEASWALVEGGISRDAELVWADLCRWVADPSQVHYWLITHKH YDHCGLLPYLCPRLPNVQVLASERTCQAWKSESAVRVVERLNRQLLRAEQRLPEACAWDALPVRAVADGEW LELGPRHRLQVIEAHGHSDDHVVFYDVRRRRLFCGDALGEFDEAEGVWRPLVFDDMEAYLESLERLQRLPT LLQLIPGHGGLLRGRLAADGAESAYTECLRLCRRLLWRQSMGESLDELSEELHRAWGGQSVDFLPGELHLG SMRRMLEILSRQALPLD

PqsH (SEQ ID NO:13)

MTVLIQGAGIAGLALAREFTKAGIDWLLVERASEIRPIGTGITLASNALTALSSTLDLDRLFRRGMPLAGI
NVYAHDGSMLMSMPSSLGGNSRGGLALQRHELHAALLEGLDESRIRVGVSIVQILDGLDHERVTLSDGTVH
DCSLVVGADGIRSSVRRYVWPEATLRHSGETCWRLVVPHRLEDAELAGEVWGHGKRLGFIQISPREMYVYA
TLKVRREEPEDEEGFVTPQRLAAHYADFDGIGASIARLIPSATTLVHNDLEELAGASWCRGRVVLIGDAAH
AMTPNLGQGAAMALEDAFLLARLWCLAPRAETLILFQQQREARIEFIRKQSWIVGRLGQWESPWSVWLRNT
LVRLVPNASRRRLHQRLFTGVGEMAAQ

PqsL (SEQ ID NO:14)

MTDNHIDVLINGCGIGGAMLAYLLGRQGHRVVVVEQARRERAINGADLLKPAGIRVVEAAGLLAEVTRRGG RVRHELEVYHDGELLRYFNYSSVDARGYFILMPCESLRRLVLEKIDGEATVEMLFETRIEAVQRDERHAID QVRLNDGRVLRPRVVVGADGIASYVRRRLLDIDVERRPYPSPMLVGTFALAPCVAERNRLYVDSQGGLAYFYPIGFDRARLVVSFPREEARELMADTRGESLRRRLQRFVGDESAEAIAAVTGTSRFKGIPIGYLNLDRYWADNVAMLGDAIHNVHPITGQGMNLAIEDASALADALDLALRDACALEDALAGYQAERFPVNQAIVSYGHALATSLEDRQRFAGVFDTALQGSSRTPEALGGERSYQPVRSPAPLG

pgsA-E operon promoter (including ATG start site of pgsA) (SEQ ID NO:15)

mvfR (SEQ ID NO:16)

ATGCCTATTCATAACCTGAATCACGTGAACATGTTCCTCCAGGTCATCGCCTCCGGTTCGATTTCCTCCGC TGCGCGGATCCTGCGCAAGTCGCACACGCGGTCAGCTCGGCGGTCAGCAACCTGGAAATCGACCTGTGCG TGGAGCTGGTCCGTCGGGACGGCTACAAGGTCGAACCCACCGAGCAGGCGCTTCGCCTGATCCCTTACATG CGCAGCCTGCTGAACTACCAGCAGCTGATCGGCGACATCGCCTTCAATCTCAACAAGGGTCCGCGCAATCT

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MvfR ((SEQ ID NO:17)

MPIHNLNHVNMFLQVIASGSISSAARILRKSHTAVSSAVSNLEIDLCVELVRRDGYKVEPTEQALRLIPYM RSLLNYQQLIGDIAFNLNKGPRNLRVLLDTAIPPSFCDTVSSVLLDDFNMVSLIRTSPADSLATIKQDNAE IDIAITIDEELKISRFNQCVLGYTKAFVVAHPQHPLCNASLHSIASLANYRQISLGSRSGQHSNLLRPVSD KVLFVENFDDMLRLVEAGVGWGIAPHYFVEERLRNGTLAVLSELYEPGGIDTKVYCYYNTALESERSFLRF LESARORLRELGRQRFDDAPAWQPSIVETAQRRSGPKALAYRQRAAPE

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(% of PA14)	mvfR	phnAB	pqsA	pqsB	pqsE	mvfR compl.	lasR
ННQ	0	48 ± 5	0	0	49 ± 4	1017 ± 247	250 ± 11
HHQ N-	0	110 ± 17	0	0.	148 ± 29	200 ± 41	45 ± 8
oxide	• -						
PQS	0	76 ± 11	. 0	0	90 ± 13	247 ± 65	23 ± 3
HNQ	0	68 ± 5	0	0	84 ± 5.	502 ± 106	551 ± 262
HNQ N-	0	91 ± 15	0	0	135 ± 20	286 ± 52	41 ± 3
oxide			•				
diHNQ	0	128 ± 21	0	0	160 ± 27	156 ± 49	19 ± 3
AA	0	90 ± 51	458 ±	188 ±	24 ± 17	0	6 ± 1
			221	102			
Pyocyanin	<10	24 ± 3	<10	<10	<10	· 177 ± 26	NT

FIGURE 12

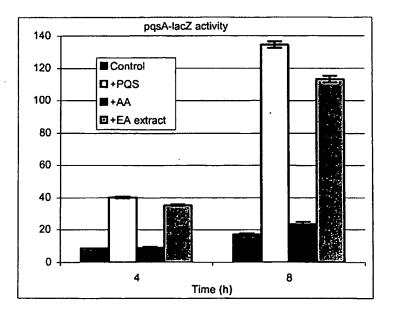
FIGURE 13

	PQS (μg/ml)	$β$ -gal activity (MU) †
lasR ⁻	2.1 ± 0.1	63.6 ± 2.6
lasR + mvfR	5.2 ± 1.8	110.5 ± 4.3
Ratio	5.0 ± 1.8	3.5 ± 0.2

FIGURE 14

	β-gal activity (MU) †				
	PA14	lasR ^{-†}			
-ННО	371 ± 8	78.7 ± 1.5			
+HHQ	473 ± 23	83.7 ± 0.2			

FIGURE 15



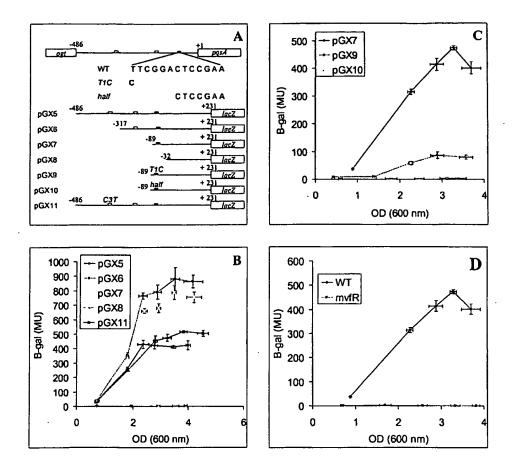


Figure 16